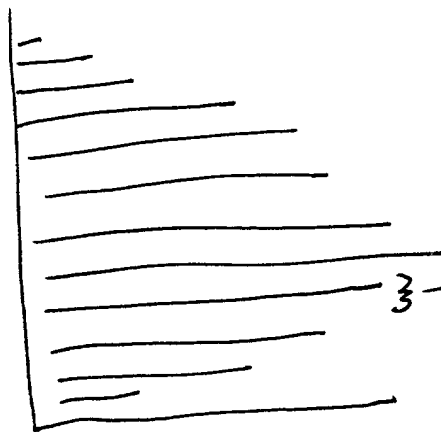


FIGURE 1

.....
.....
..... Total Genome

↓ RE Digest / Separate by length STEP 1



3 — subset of interest

STEP 2

STEP 3

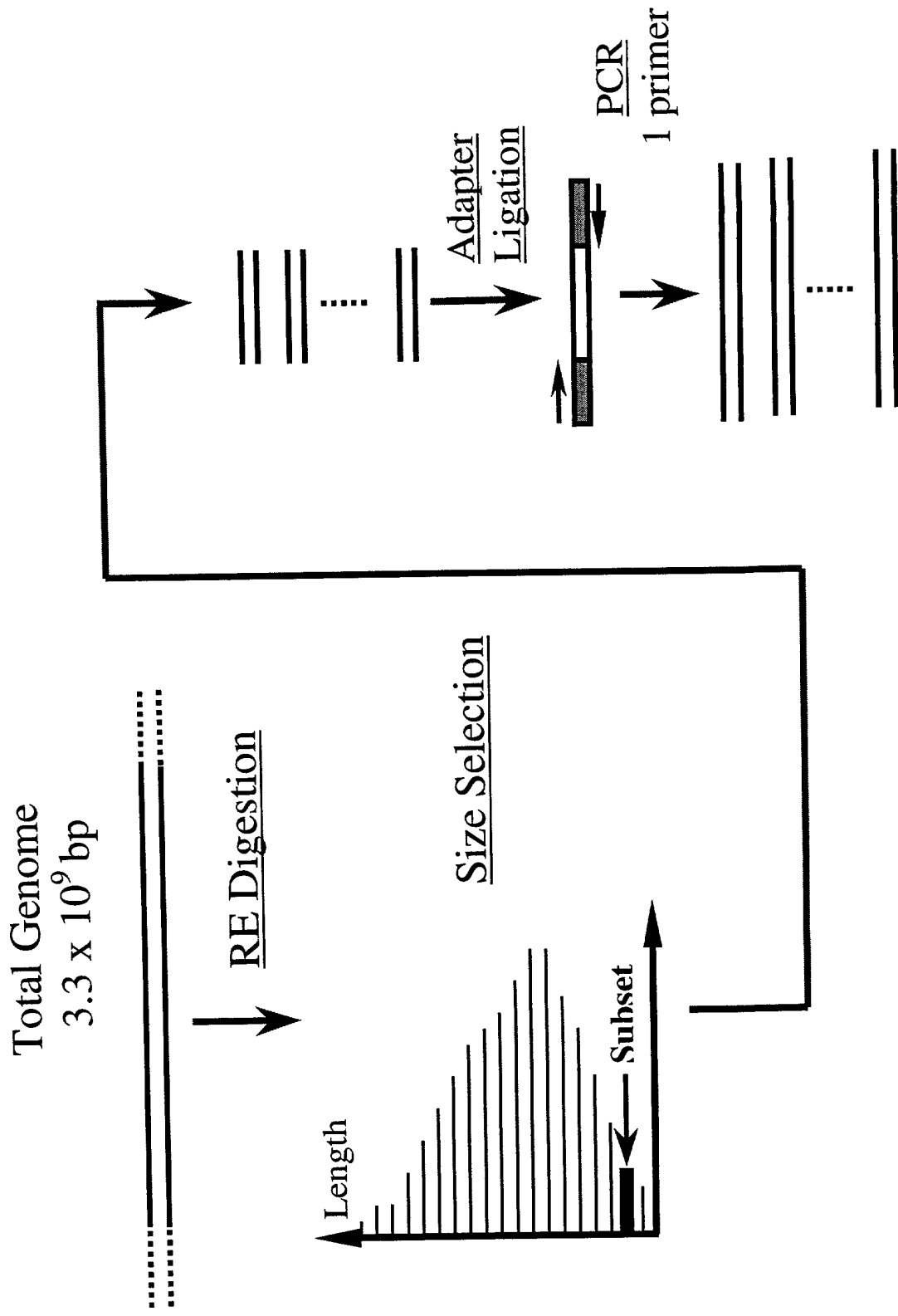
↓ purification

STEP 4

———— Isolated fragments STEP 5

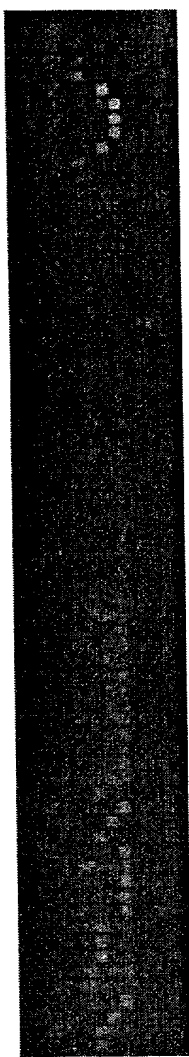
Figure 2

Figure 2: Library Construction



Effects of Complexity

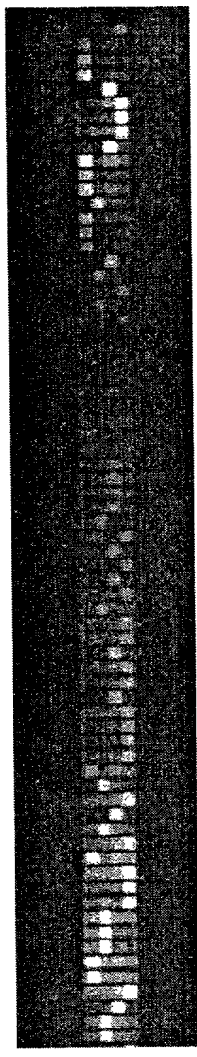
(A, C, G, T)-HGE250-350; ~16Mb



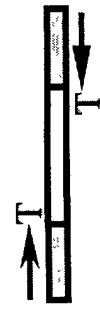
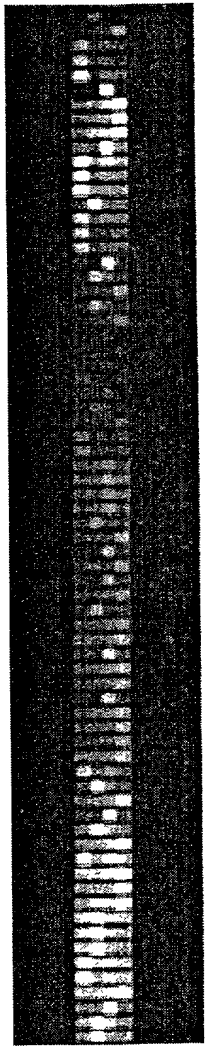
PCR Primer



(A, T)-HGE250-350; ~4Mb



(T)-HGE250-350; ~1Mb



● FIGURE 4

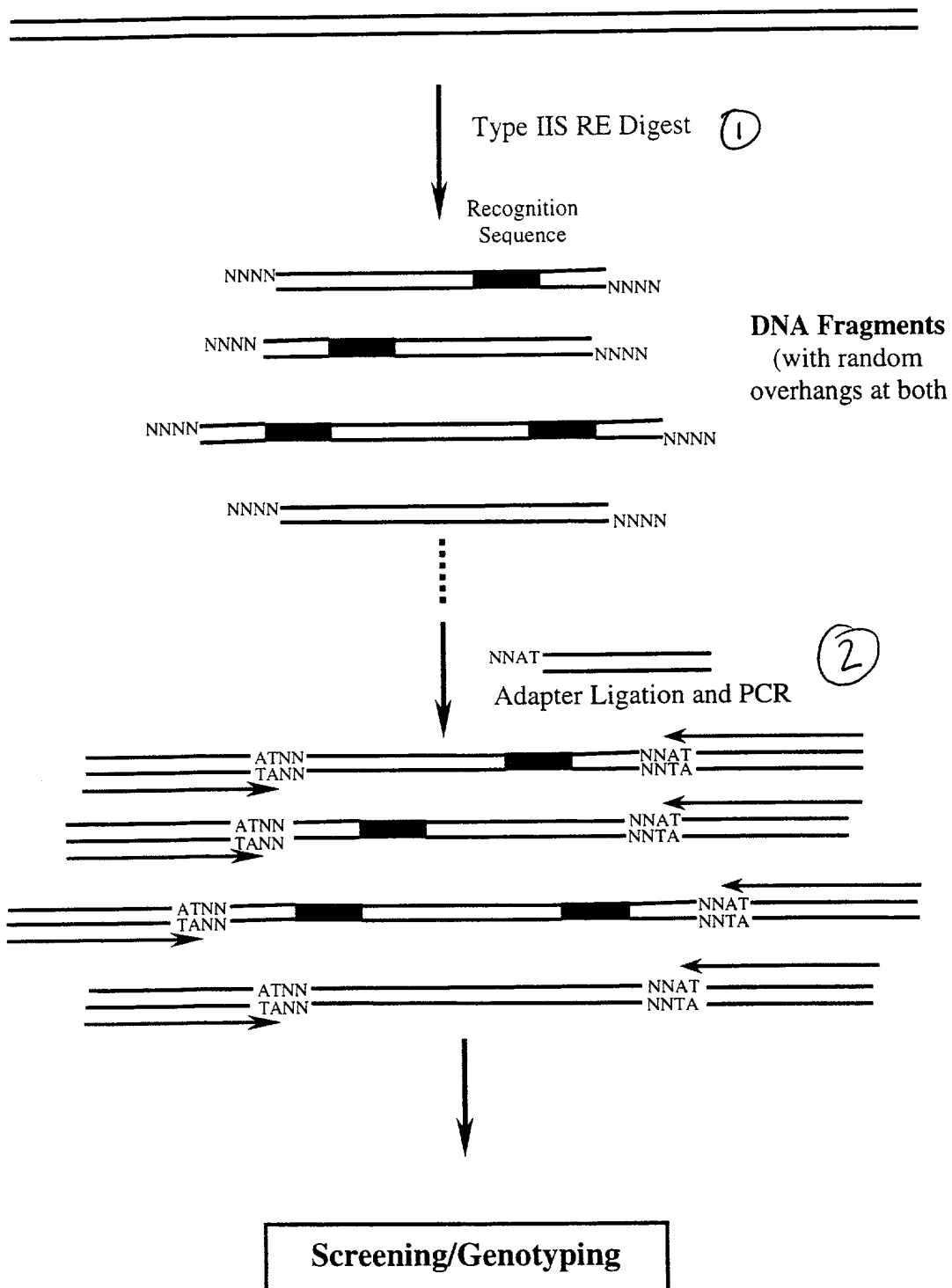


FIGURE 5


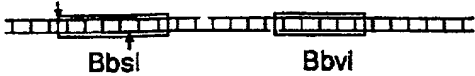
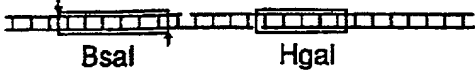
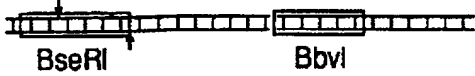
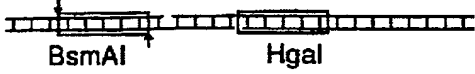
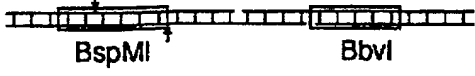

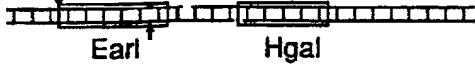
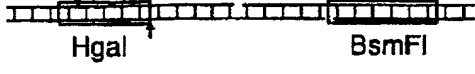
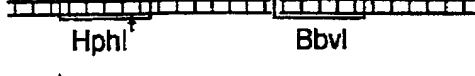

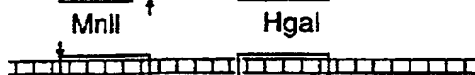
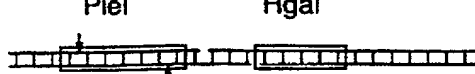


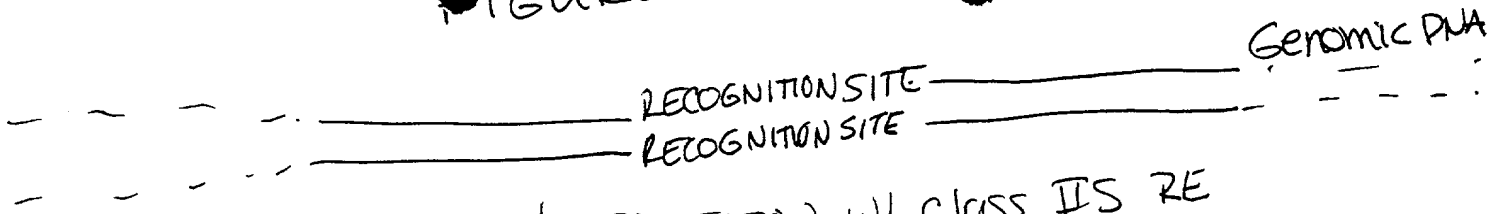
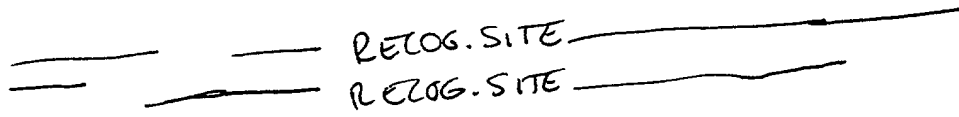
	cleavage Frequency of first enzyme	sites in λ	size of captured sequence (bp)
	1/512	58	5
	1/2048	24	6
	1/2048	2	5
	1/2048	19	8
	1/512	37	5
	1/2048	41	8
	1/2048	14	5
	1/2048	34	4
	1/512	102	10
	1/512	168	7
	1/512	130	7
	1/128	262	6
	1/512	61	5
	1/8192	10	4
	1/512	169	9

Fig. 1

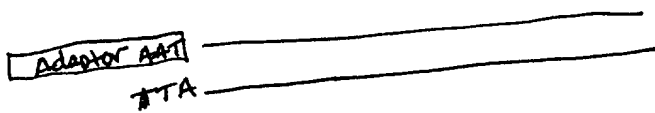
FIGURE 6



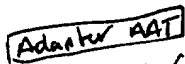
↓ DIGESTION w/ class II RE



↓ ligation



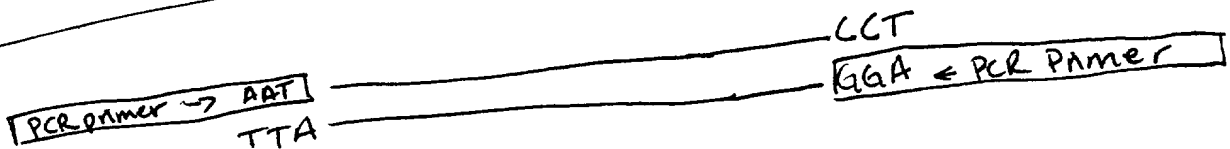
ligation



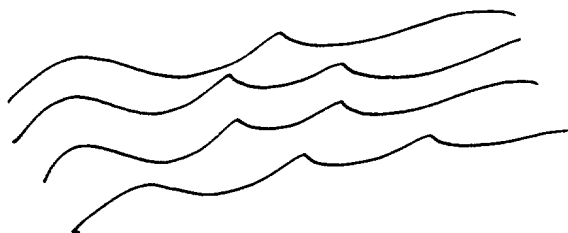
CTT

no ligation

A.



↓ amplification

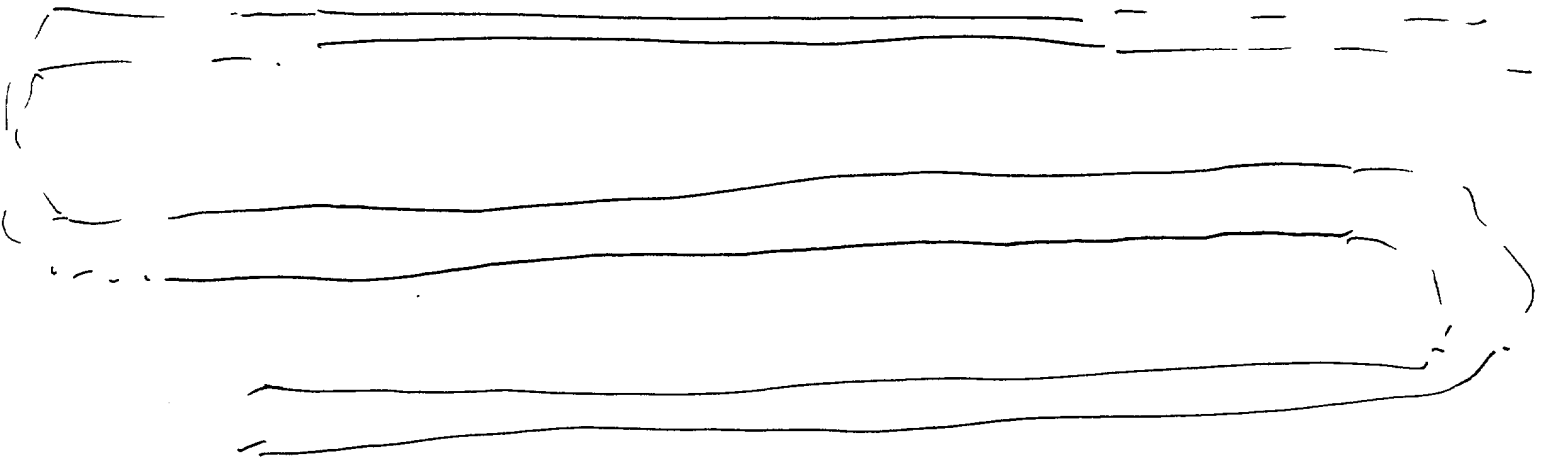


CCT AAG not amplified

B.

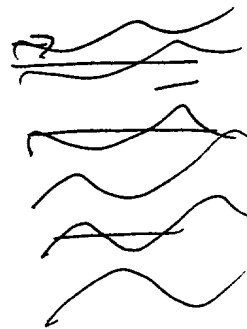
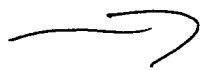
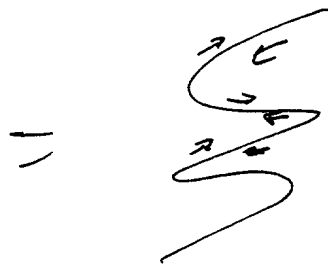
● Figure 7 ●

total genomic DNA



*nncgttga →

←nnnnngc



Complexity of AP Amplified Human Genomic DNA

Primer	Sequence	Annealing T	Polymerase	# Present	%
Total Genome				434	6.1
sdp5	nncgttgg	30	ThermoSequenase	393	5.6
sdp3	agagctgc	30	TaqGold	264	3.7
DOP	ccgactcgagnnnnnnatgtgg	30	TaqGold	247	3.5
sdp8	nnnnnnngccgttgg	45	TaqGold	218*	3.1*
sdp8-10	nnnnnatgccgttgg	45	TapGold	206	2.9
sdp8	nnnnnnngccgttgg	55	TaqGold	114	1.6

* Results of 20 µg/200µl hybridization.

Reproducibility of AP PCR

Independent preps of sdp8/H.G. DNA(B.M.)/45°C

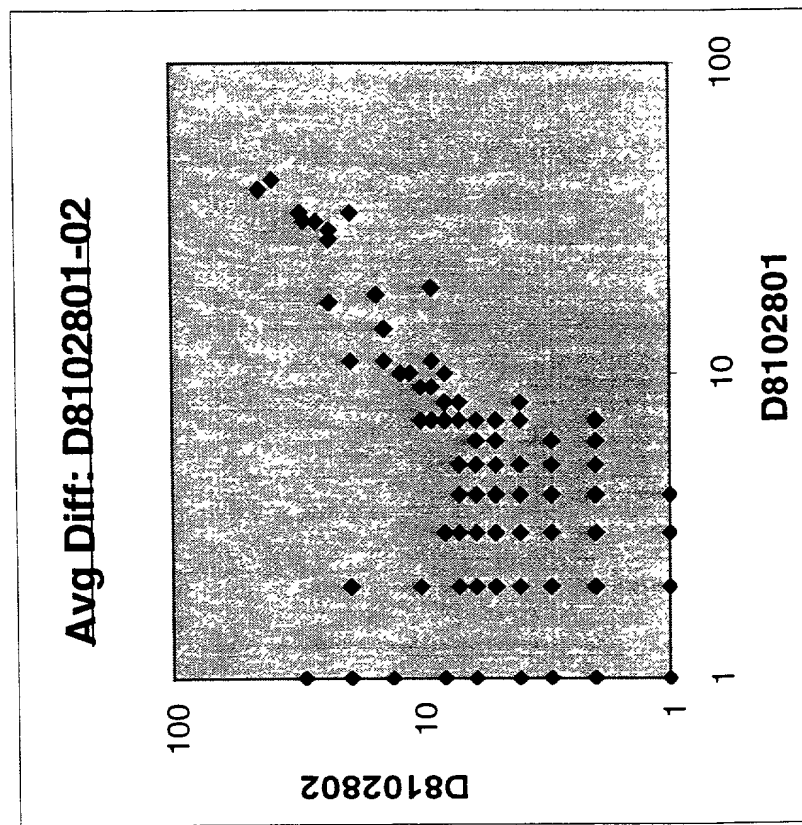
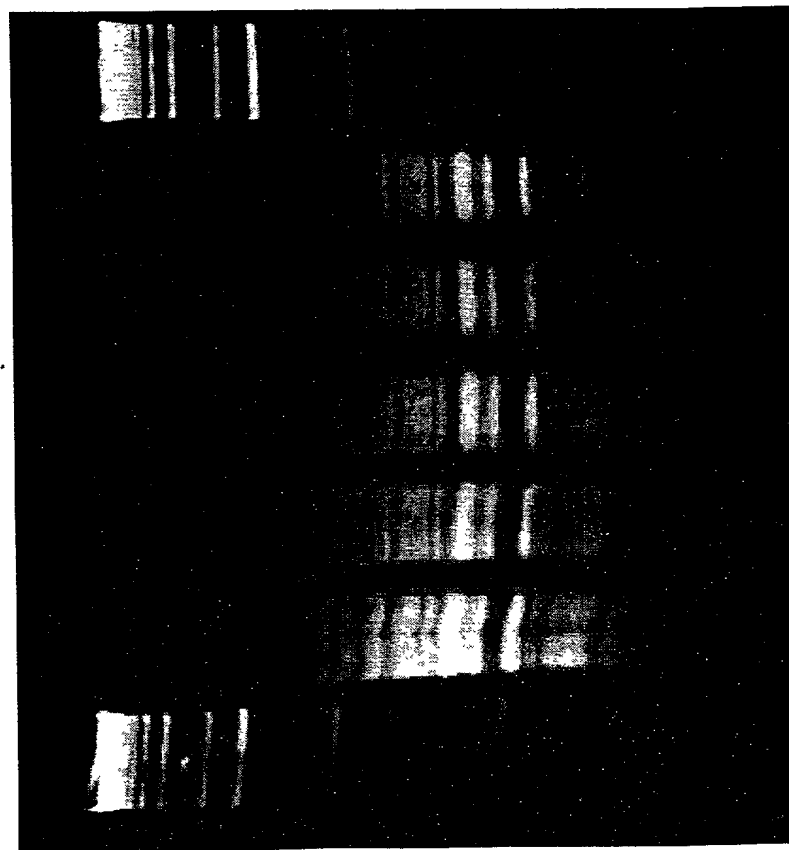
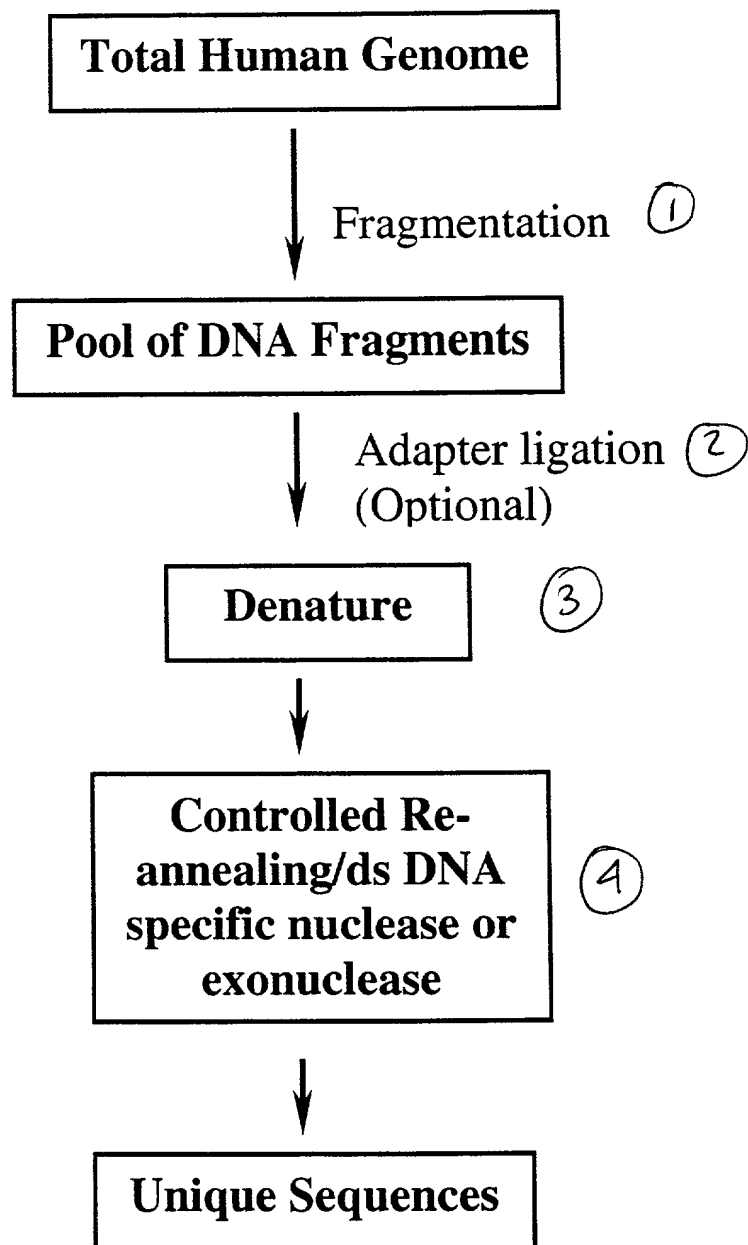


FIGURE 10

A Novel Way of Removing repetitive sequences from Genomic DNA



Scheme IV

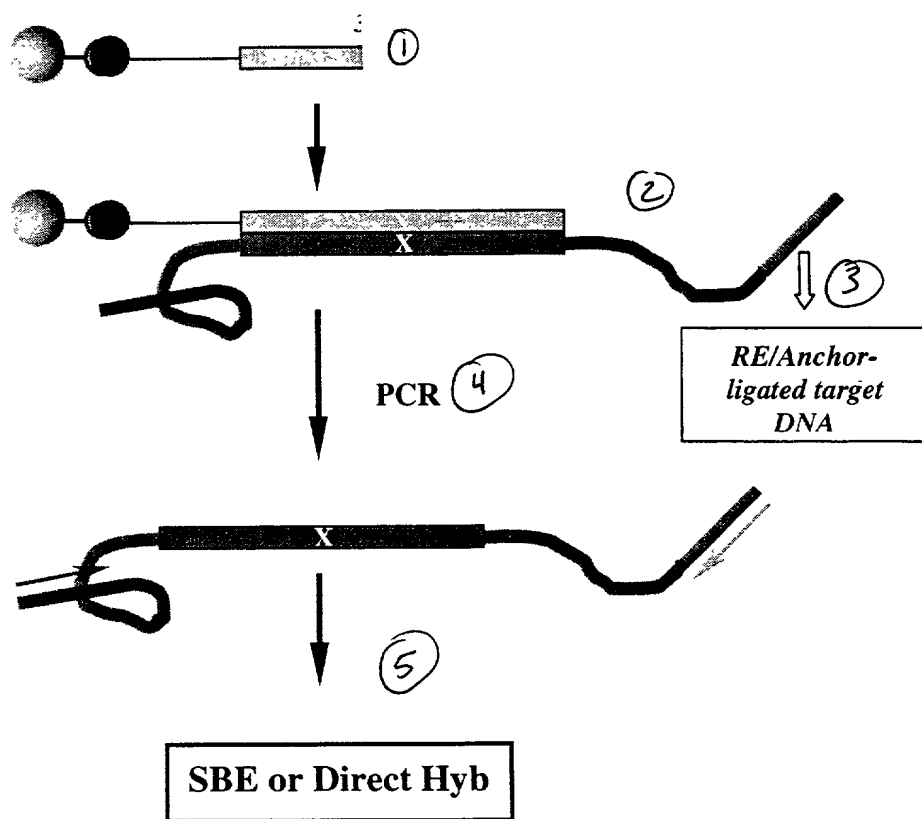


Figure 12

Scheme I

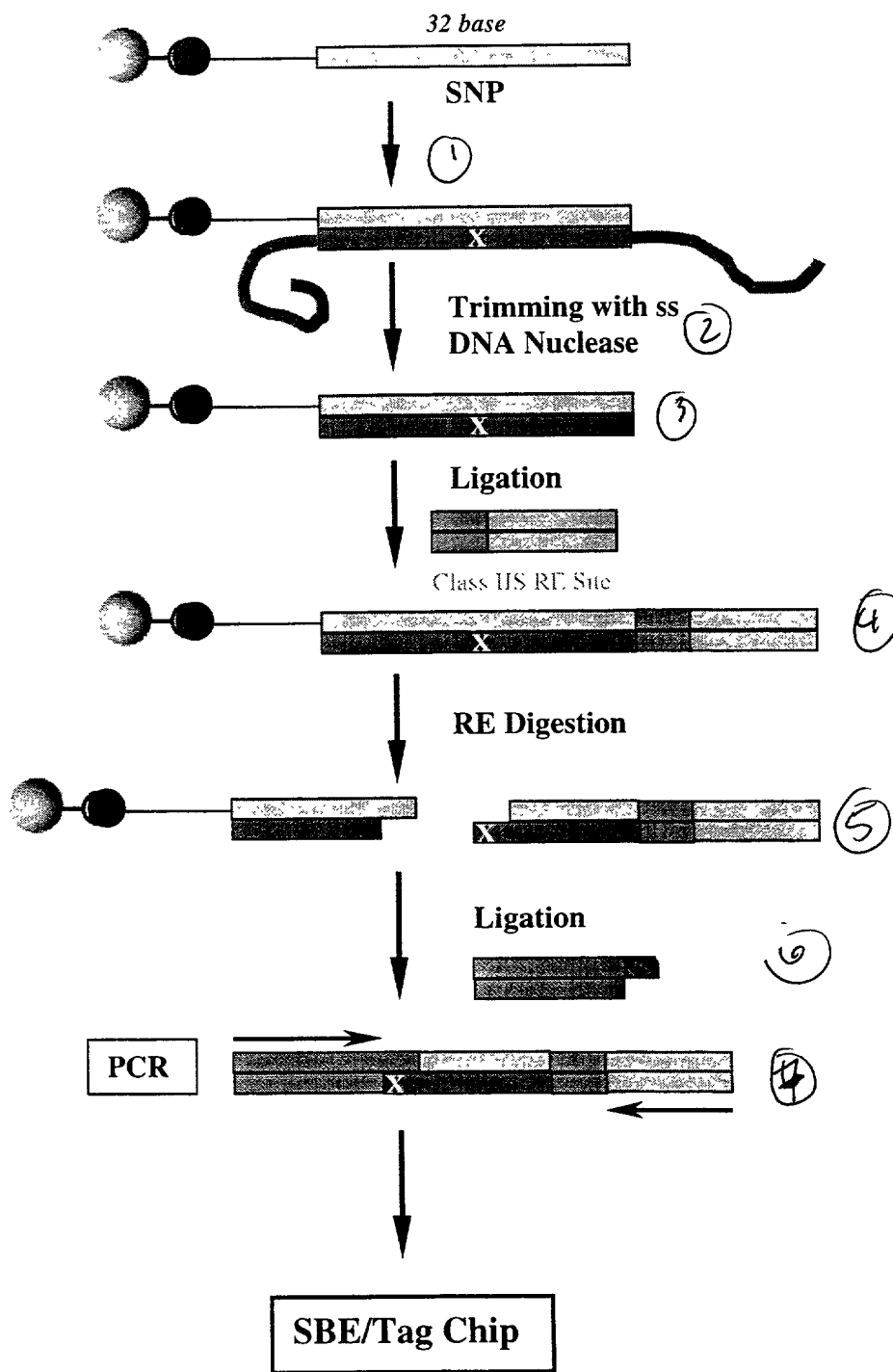


Figure 13

Scheme III

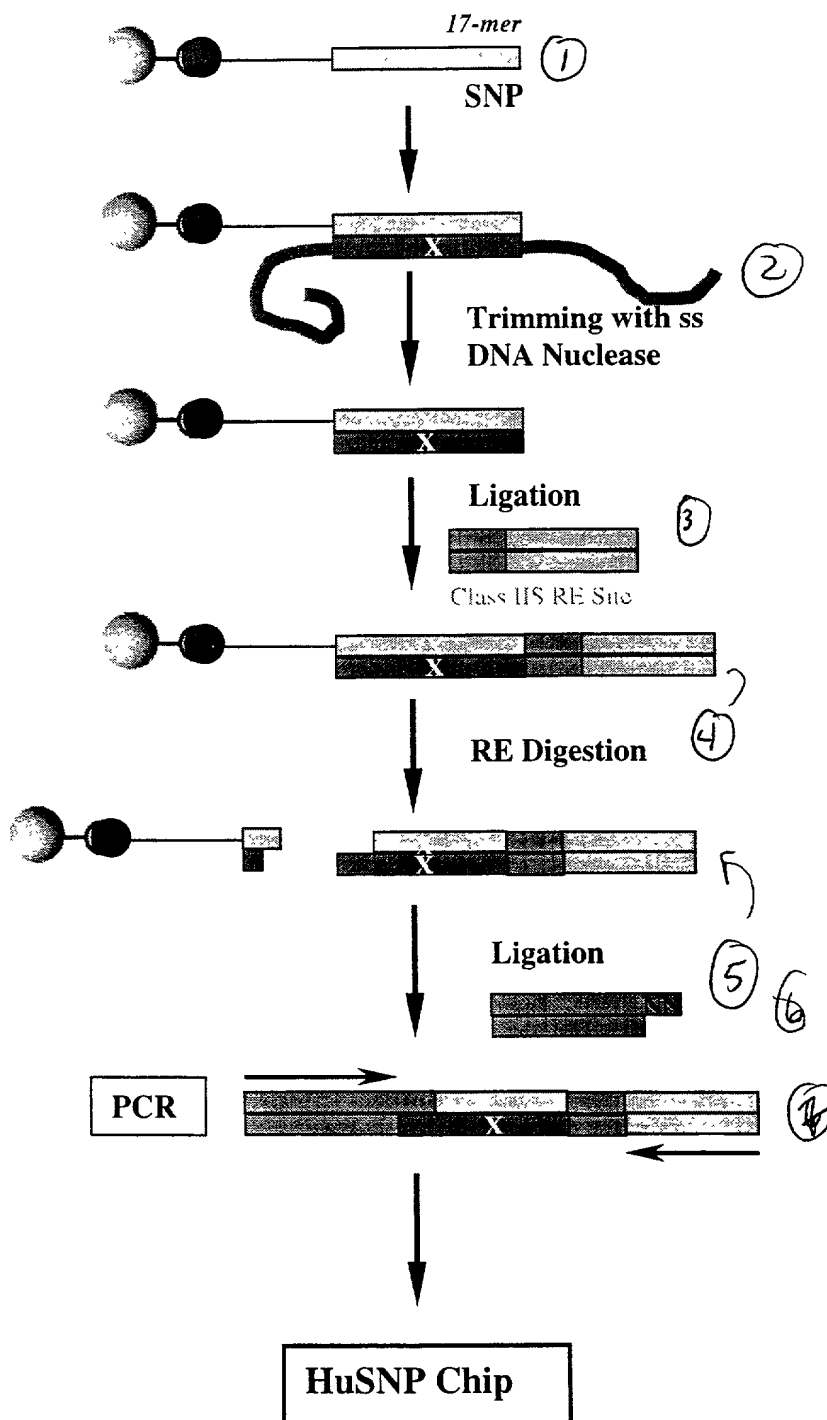


FIGURE 14

Chimeric Probe Array

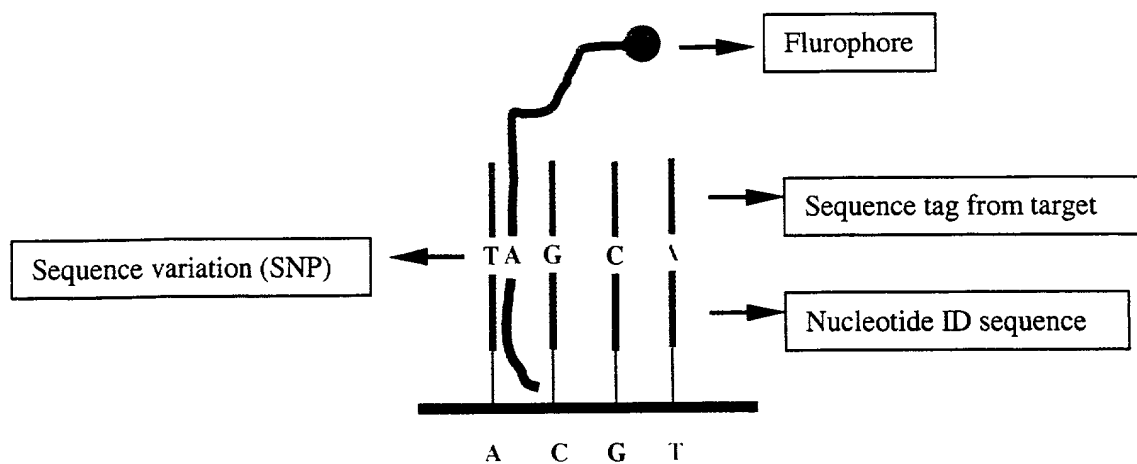


FIGURE 15

Scheme II

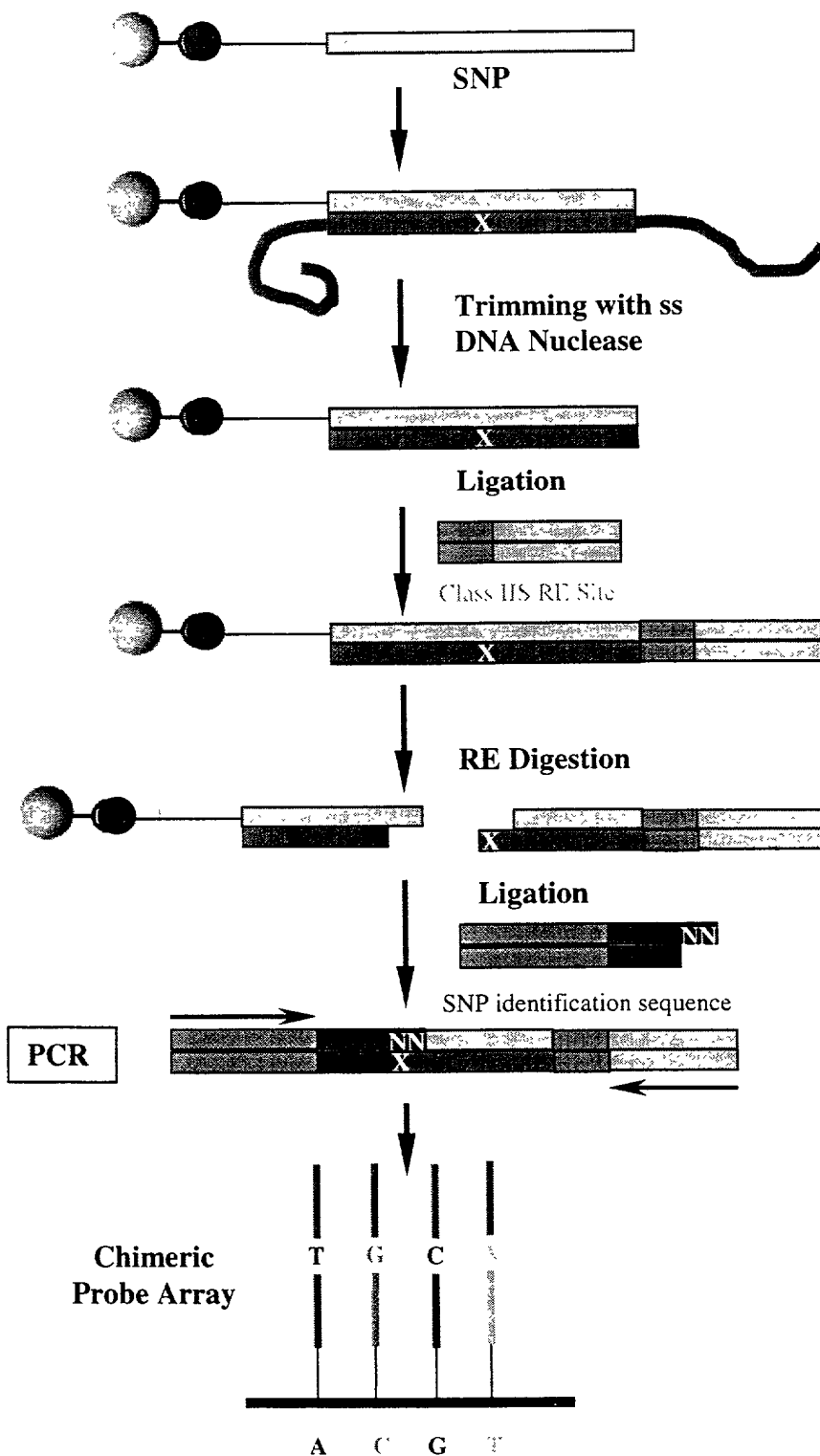
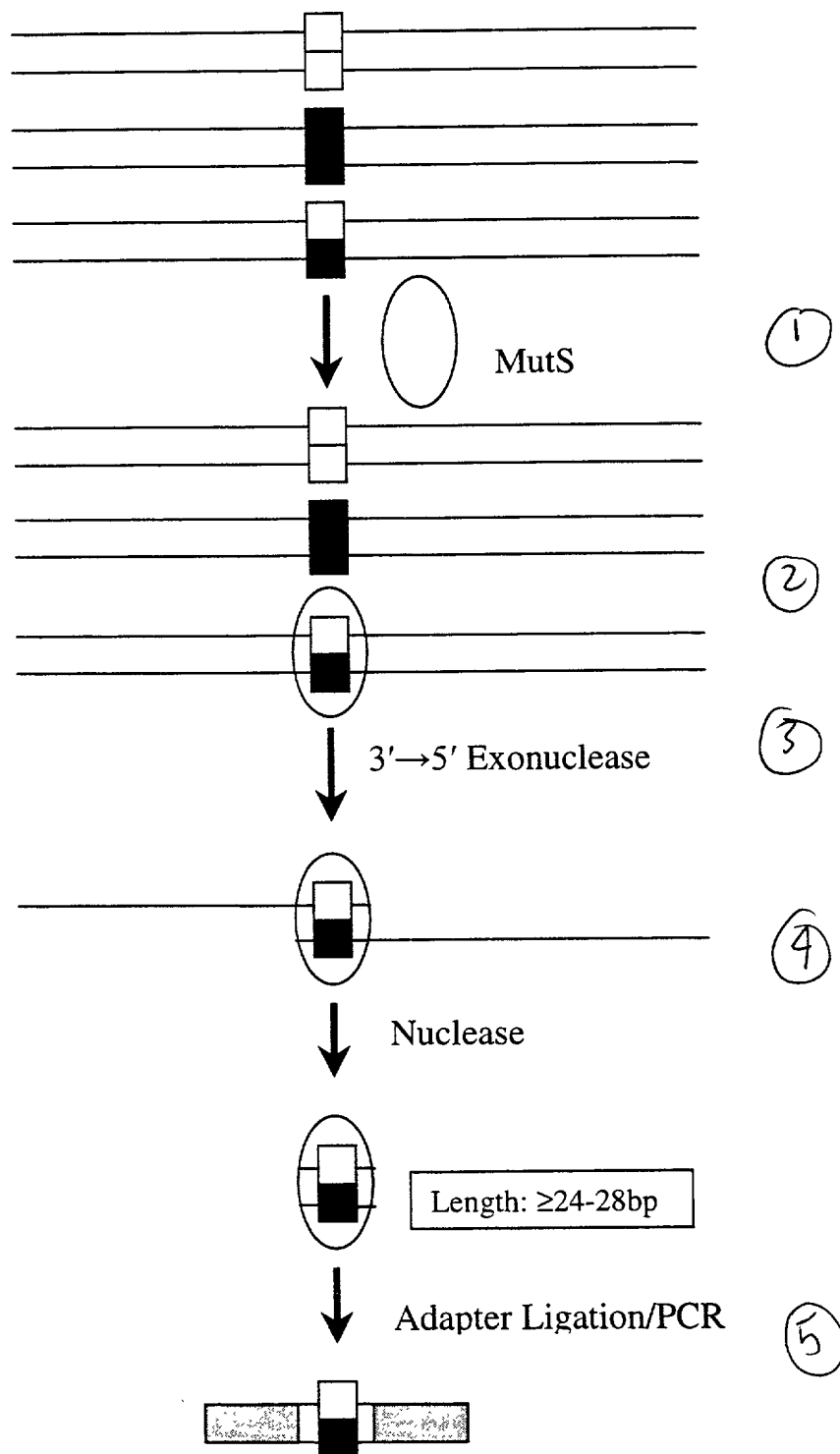


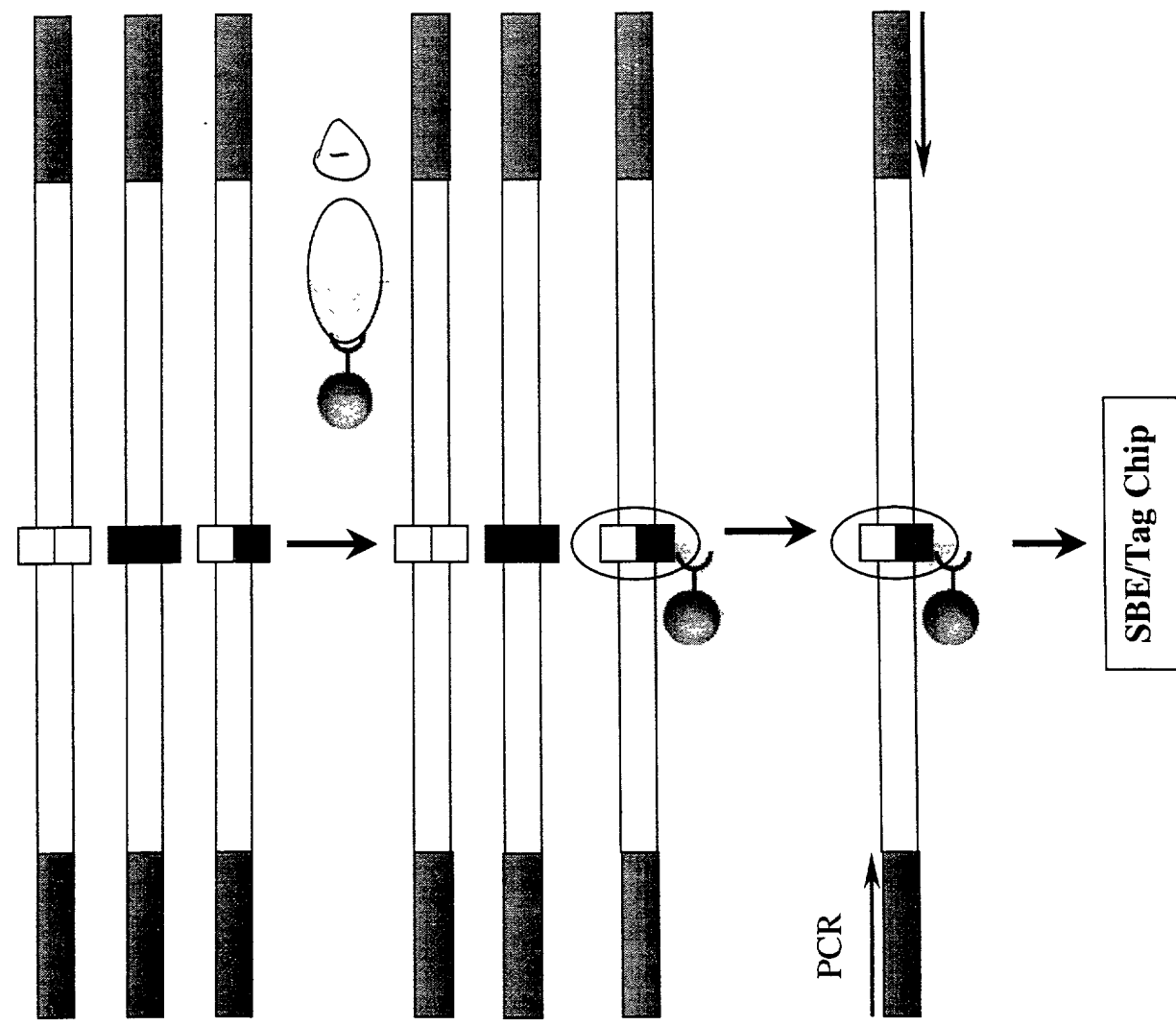
FIGURE 16

Enrichment of SNPs with MutS Protein

Scheme 1



Scheme II



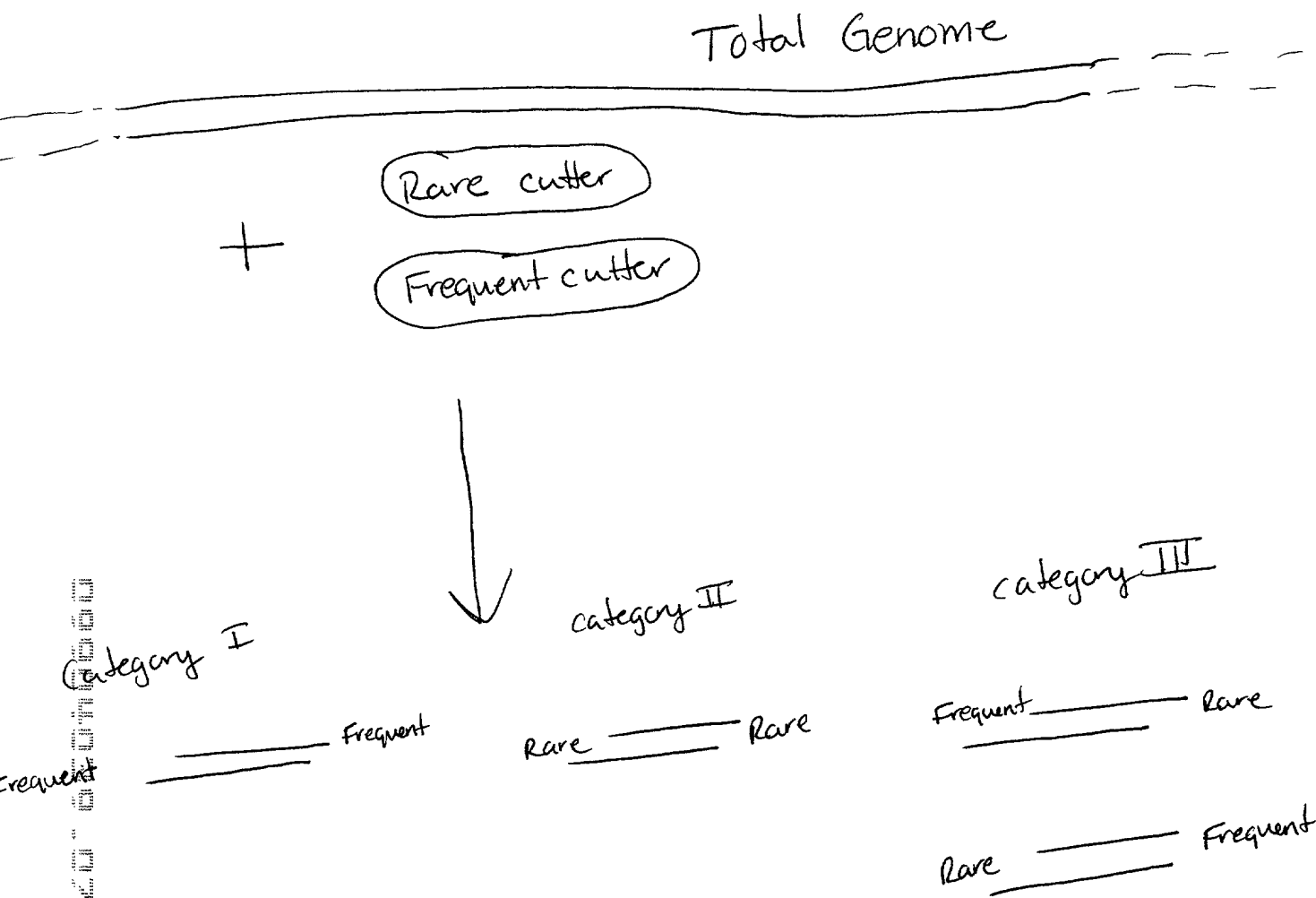
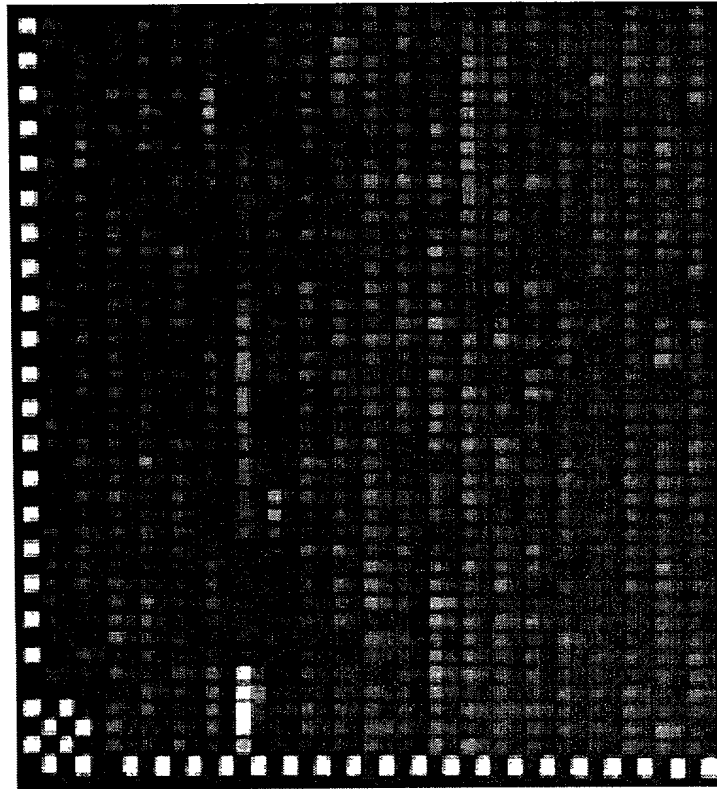


Figure 19
Total Yeast Genome

Total Yeast Genome/Y6321D
10µg/200µl



YGE250-350/Y6321D
5.24µg/200µl

